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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2011; month=10; day=6; hr=14; min=47; sec=18; ms=814;]

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Application No: 10594189 Version No: 1.0

Input Set:**Output Set:**

Started: 2011-09-29 15:43:17.530
Finished: 2011-09-29 15:43:21.703
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 173 ms
Total Warnings: 41
Total Errors: 0
No. of SeqIDs Defined: 41
Actual SeqID Count: 41

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2011-09-29 15:43:17.530
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Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 173 ms
Total Warnings: 41
Total Errors: 0
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Actual SeqID Count: 41

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Universitaet Stuttgart
 PFIZENMAIER, Klaus
 SCHEURICH, Peter
 GRUNWALD, Ingo
 KRIPPNER-HEIDENREICH, Anja

<120> RECOMBINANT POLYPEPTIDES OF THE MEMBERS OF THE TNF LIGAND FAMILY AND USE THEREOF

<130> 040045-0358701

<140> 10594189

<141> 2011-09-29

<150> PCT/EP2005/003158

<151> 2005-03-24

<150> DE 102004014983.6-4

<151> 2004-03-26

<160> 41

<170> PatentIn version 3.3

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence Sequence

<220>

<223> Description of Artificial Sequence: Synthetic flag-tag peptide sequence

<400> 1

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 2

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide linker sequence

<400> 2

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide linker sequence

<400> 3

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 4

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker sequence

<400> 4

ggtggcggtt ctggtggcgg ttctggtggc ggatcc 36

<210> 5

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Linker sequence

<400> 5

ggtggcggtt ctggtggcgg ttctggtggc ggttctggtg gcggatcc 48

<210> 6

<211> 84

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF Primer I

<400> 6

tcgattaagc ttcccggggg atccgccacc agaaccgccca ccagaaccgc caccagagc 60

gatgataccg aagtaaacct gacc 84

<210> 7

<211> 97

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: scTNF Primer II

<400> 7
atcgattaag cttcccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60

cgccaccag agcgatgata ccgaagtaaa cctgacc 97

<210> 8
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTNF Primer III

<400> 8
ccccgaattc ggatcctctt ctcgtacccc gtctgacaaa ccg 43

<210> 9
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTNF Primer IV

<400> 9
ggggggggaag cttatcgata gttagatatc atcacagagc gatgataccg aag 53

<210> 10
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: scTNF Primer V

<400> 10
cctgtacctg atctactccc aggttctgtt caaaggccag g 41

<210> 11
<211> 97
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: cys-scTNF Primer VI

<400> 11
aattcattaa agaggagaaa ttaactatgg gagagctcat cgaaggtcgc tgcgccggtg 60

gatctggtca tcatcatcac catcacggct cagacgg 97

<210> 12

<211> 97
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: cys-scTNF Primer VII

 <400> 12
 cgctccgtct gagccgtgat ggtgatgatg atgaccagat ccaccggcgc agcgaccttc 60

 gatgagctct cccatagtta atttctcttc tttaatg 97

 <210> 13
 <211> 100
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer FasL#1R

 <400> 13
 atcgatttct agaccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60

 cgccaccgag cttatataag ccgaaaaacg tctgagattc 100

 <210> 14
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer FasL#2F

 <400> 14
 ggggtagcgg ccgcgctgtc gacgattaca aagac 35

 <210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer FasL#3F

 <400> 15
 agaaaaaaag gagctgagga aagtgg 26

 <210> 16
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: Primer FasL#4F

<400> 16
ggggcgatc cgaaaaaag gagctgagga aagtgg 36

<210> 17
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer FasL#5R

<400> 17
ggggcctcta gaatcgatgg tcagagctta tataagccga aaaacgtctg 50

<210> 18
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer HA-IF

<400> 18
cgccatggct atcatctacc tcatcctcct gttcacogct gtgcggggag c 51

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer HA-IIR

<400> 19
ggccgctgcc ccgcacagcg gtgaacagga ggatgaggta gatgatagcc atggcggtac 60

<210> 20
<211> 106
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer TRAIL#1R

<400> 20
atcgatttct agaccgggg gatccgccac cagaaccgcc accagaaccg ccaccagaac 60

cgccaccgcc aactaaaaag gccccgaaaa aactggcttc atggtc 106

<210> 21

<211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#2F

 <400> 21
 ggggtagaat tcggaacctc tgaggaaacc atttctacag ttcaag 46

 <210> 22
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#3F

 <400> 22
 aacctctgag gaaaccattt ctacag 26

 <210> 23
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#4F

 <400> 23
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 <210> 24
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer TRAIL#5R

 <400> 24
 ggggcctcta gaatcgatgg tcagccaact aaaaaggccc cgaaaaaact ggc 53

 <210> 25
 <211> 1506
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: sCTNF-L short chain

 <220>

<221> CDS

<222> (1)..(1503)

<400> 25

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Met Arg Gly Ser His His His His His Gly Ser Ala Ser Ser Ser	
1 5 10 15	

tct cgt acc ccg tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg	96
Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro	
20 25 30	

cag gct gaa ggt caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg	144
Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu	
35 40 45	

ctg gct aac ggt gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct	192
Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser	
50 55 60	

gaa ggc ctg tac ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc	240
Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly	
65 70 75 80	

tgc ccg tcc acc cac gtt ctg ctg acc cac acc atc tct cgt atc gct	288
Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala	
85 90 95	

gtt tcc tac cag acc aaa gta aac ctg ctg tct gca atc aaa tct ccg	336
Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro	
100 105 110	

tgc cag cgt gaa acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa	384
Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu	
115 120 125	

ccg atc tac ctg ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg	432
Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu	
130 135 140	

tct gca gaa att aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt	480
Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly	
145 150 155 160	

cag gtt tac ttc ggt atc atc gct ctg ggt ggc ggt tct ggt ggc ggt	528
Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly	
165 170 175	

tct ggt ggc gga tcc tct tct cgt acc ccg tct gac aaa ccg gtt gct	576
Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala	
180 185 190	

cac gtt gtt gca aac ccg cag gct gaa ggt caa ctg caa tgg ctg aac	624
His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn	
195 200 205	

cgt cgt gct aac gct ctg ctg gct aac ggt gtt gaa ctg cgt gac aac	672
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Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn	
210 215 220	
cag ctg gtt gtt ccg tct gaa ggc ctg tac ctg atc tac tcc cag gtt	720
Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val	
225 230 235 240	
ctg ttc aaa ggc cag ggc tgc ccg tcc acc cac gtt ctg ctg acc cac	768
Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His	
245 250 255	
acc atc tct cgt atc gct gtt tcc tac cag acc aaa gta aac ctg ctg	816
Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu	
260 265 270	
tct gca atc aaa tct ccg tgc cag cgt gaa acc ccg gaa ggt gct gaa	864
Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu	
275 280 285	
gct aaa ccg tgg tac gaa ccg atc tac ctg ggt ggc gtt ttt caa ctg	912
Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu	
290 295 300	
gag aaa ggt gac cgt ctg tct gca gaa att aac cgt ccg gac tac ctg	960
Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu	
305 310 315 320	
gac ttc gca gaa tct ggt cag gtt tac ttc ggt atc atc gct ctg ggt	1008
Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly	
325 330 335	
ggc ggt tct ggt ggc ggt tct ggt ggc gga tcc tct tct cgt acc ccg	1056
Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro	
340 345 350	
tct gac aaa ccg gtt gct cac gtt gtt gca aac ccg cag gct gaa ggt	1104
Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly	
355 360 365	
caa ctg caa tgg ctg aac cgt cgt gct aac gct ctg ctg gct aac ggt	1152
Gln Leu Gln Trp Leu Asn Arg Ala Asn Ala Leu Leu Ala Asn Gly	
370 375 380	
gtt gaa ctg cgt gac aac cag ctg gtt gtt ccg tct gaa ggc ctg tac	1200
Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr	
385 390 395 400	
ctg atc tac tcc cag gtt ctg ttc aaa ggc cag ggc tgc ccg tcc acc	1248
Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr	
405 410 415	
cac gtt ctg ctg acc cac acc atc tct cgt atc gct gtt tcc tac cag	1296
His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln	
420 425 430	
acc aaa gta aac ctg ctg tct gca atc aaa tct ccg tgc cag cgt gaa	1344
Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu	

435

440

445

acc ccg gaa ggt gct gaa gct aaa ccg tgg tac gaa ccg atc tac ctg 1392
 Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
 450 455 460

ggt ggc gtt ttt caa ctg gag aaa ggt gac cgt ctg tct gca gaa att 1440
 Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
 465 470 475 480

aac cgt ccg gac tac ctg gac ttc gca gaa tct ggt cag gtt tac ttc 1488
 Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe
 485 490 495

ggt atc atc gct ctg tga 1506
 Gly Ile Ile Ala Leu
 500

<210> 26

<211> 501

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sctNF-L short chain peptide

<400> 26

Met Arg Gly Ser His His His His His His Gly Ser Ala Ser Ser Ser
 1 5 10 15

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
 20 25 30

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
 35 40 45

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
 50 55 60

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
 65 70 75 80

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
 85 90 95

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
 100 105 110

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
115 120 125

Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
130 135 140

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
145 150 155 160

Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly Gly Gly Ser Gly Gly Gly
165 170 175

Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala
180 185 190

His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn
195 200 205

Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn
210 215 220

Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val
225 230 235 240

Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His
245 250 255

Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu
260 265 270

Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu
275 280 285

Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu
290 295 300

Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu
305 310 315 320

Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu Gly
325 330 335

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ser Arg Thr Pro

340

345

350

Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly
355 360 365

Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
370 375 380

Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
385 390 395 400

Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
405 410 415

His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
420 425 430

Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
435 440 445

Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
450 455 460

Gly Gly Val Phe Gln Leu Glu Lys